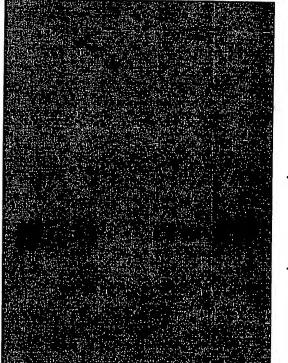
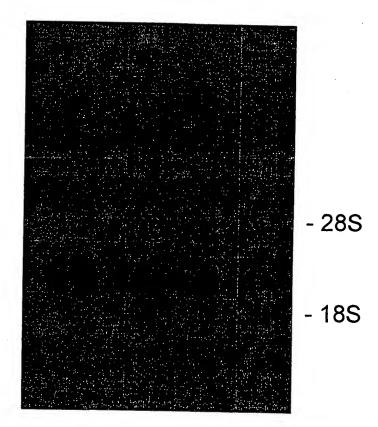
FIG. 1A



- 28S

- 18S

F/G.1B

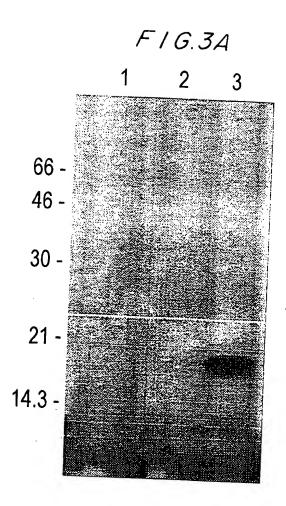


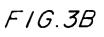


F1G. 2

CTGGCTGCTGTGGAGTTTGTGACATACTAGGTGACACCCTTGGAGTCACTTCTCTCAACTCCAGCTTAGAAGTGCCTGCC

- 233 ATGGAGGTGGCGGTCTATCAGCTGCACAATTTCTCCACCTCCTTCTTTTCTTCTGCTT ${\tt MetGluValAlaValTyrGlnLeu} {\tt HisAsnPheSerThrSerPhePheSerSerLeuLeu}$
- 293 GGAGGGGATGTGGTTTCCGTTAAACTGGATAACAGTGCCTCCGGAGCCAGTGTGGTGGCC GlyGlyAspValValSerValLysLeuAspAsnSerAlaSerGlyAlaSerValValAla
- 353 CTAGACAACAAGATTGAGCAGGCCATGGACCTCGTGAAGAACCACCTGATGTACGCTGTG LeuAspAsnLyaIleGluGlnAlaMetAspLeuValLyaAsnHiaLeuMetTyrAlaVal
- 413 AGAGAGGAGGTGGAGGTCCTAAAGGAGCAGATTCGTGAGCTGCTTGAGAAGAACTCCCAG ${\tt ArgGluGluValGluValLeuLysGluGlnIleArgGluLeuLeuGluLysAsnSerGln}$
- 473 CTGGAGCGCGAGAACACCCTCCTGAAGACGCTGGCAAGCCCCGAGCAACTGGAAAAGTTC LeuGluArgGluLeuThrLeuLeuLysThrLeuAlaSerProGluGlnLeuGluLysPhe
- 533 CAGTCCCGGCTGAGCCCTGAAGACCCCGGAAACCCCGGAAACCCCG ${\tt GlnSerArgLeuSerProGluGluProAlaProGluAlaProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProGluThrProG$
- 593 GAAGCCCCTGGTGGTTCTGCGGTGTAAGTGGCTCTGTCCTTAGGGTGGGCAGAGCCACAT GluAlaProGlyGlySerAlaVal *
- 653 CTTGTTCTACCTAGTTCTTTCCAGTTTGTTTTTTGGCTCCCCAAGGGTCATCTCATGTGGA 713 GAACTTTACACCTAACATAGCTGGTGCCAAGAGATGTCCCAAGGACATGCCCATCTGGGT 773 CCACTCCAGTGACAGACCCCTGACAAAGAGCAGGTCTCTGGAGACTAAGTTGCATGGGGC 833 CTAGTAACACCAAGCCAGTGAGCCTGTCGTGTCACCGGGCCCTGGGGGCTCCCAGGGCTG
- 893 GGCAACTTAGTTACAGCTGACCAAGGAGAAAGTAGTTTTGAGATGTGATGCCAGTGTGCT 953 CCAGAAAGTGTAAGGGGTCTGTTTTCATTTCCATGGACATCTTCCACAGCTTCACCTGA
- 1073 TCCTCTGTCTTTTCCAGGCAGGGCCAGAGATGGGGAGAGATTGAGCCAAATGAGCCTTCTG
- 1113 TTGGTTAATACTGTATAATGCATGGCTTTGTGCACAGCCCAGTGTGGGGTTACAGCTTTG
- 1193 GGATGACTGCTTATAAAGTTCTGTTTGGTTAGTATTGGCATCGTTTTTCTATATAGCCAT 1253 AATGCGTATATATACCCATAGGGCTAGATCTATATCTTAGGGTAGTGATGTATACATATA
- 1373 CTCTTAAAGCTAAGTTTTTGACTGTGCTAATTTACCAAATTGATCCAGTTTGTCCTTTAG
- 1433 ATTANATANGACTCGATATGAGGGAGGGGAGGGGAAGACCAGCCTCACAATGCGGCCACAG 1493 ATGCCTTGCTGCAGTCCTCCCTGATCTGTCCACTGAAGACATGAAGTCCTCTTTTGA
- 1553 ATGCCAAACCCACCATTCATTGGTGCTGACTACATAGAATGGGGTTGAGAGAAGATCAGT
- 1673 TTGTTTGTTTTTTTTTTTTTTTTTTTTTTTTAAGTTCTTGTGGGGAAACTTTGGG
- 1733 GTTAATCAAAGGATGTAGTCCTGTGGTAGACCAGAGGAGTAACTAGTTTTGATCCTTTGG
- 1793 GGTGTGGAAAATGTACCCAGGAAGCTTGTGTAAGGAGGTTCTGTGACAGTGAACACTTTC
- 1953 COCTTTCTGACACCTCATCCTGCTACGACTCCAGGATTTGGATTTGGATTTTCAAAT





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FIG.3C 1 2 3 4

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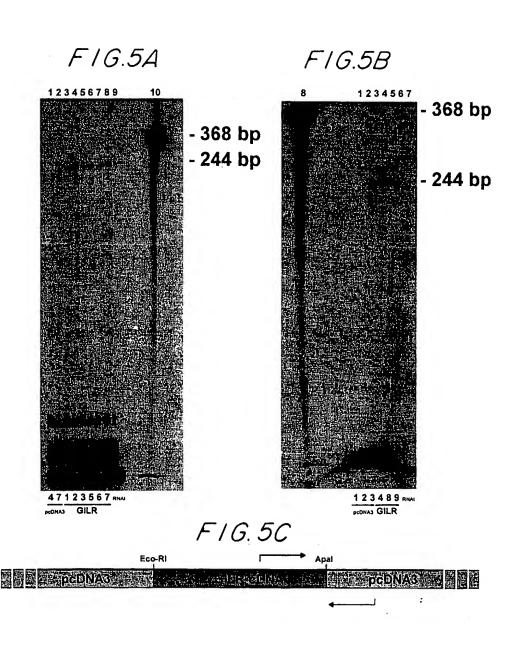
21 -

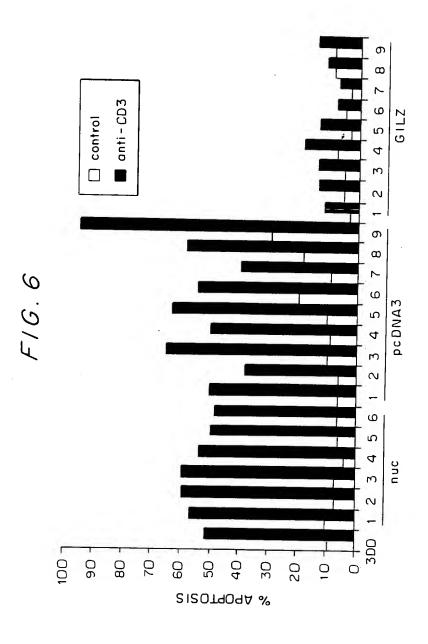
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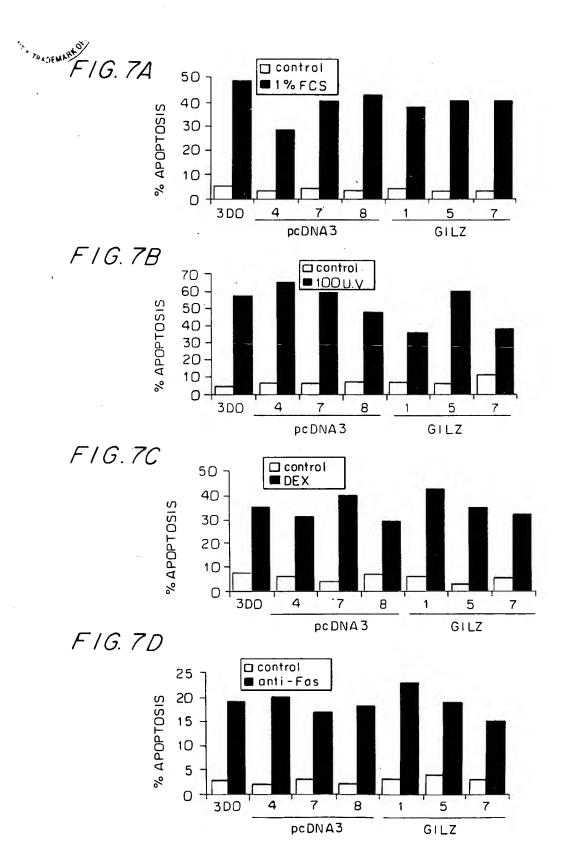


GILR	L K E Q I R E L L E K N S Q L E R E N T L L	KTLA
TSC-22	LKEQIKELIEKNSQLEQENDLL	KTLA
GCN4	LEDKVEELLSKNYHLENEVARL	KKLV
CREB	LENRVAVLENQNKTLIEELKAL	KDLY
CREM	LENRVAVLENQNKTLIEELKAL	KDLY
c-jun	LEEKVKTLKAQNSELASTANML	REQV

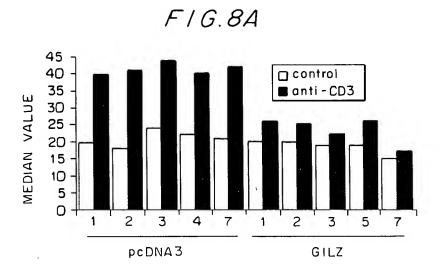
F1G.4











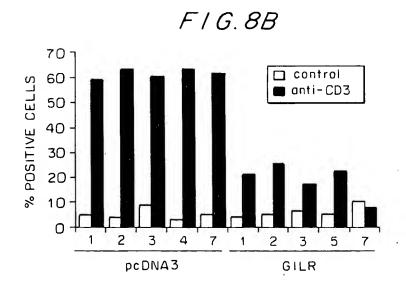
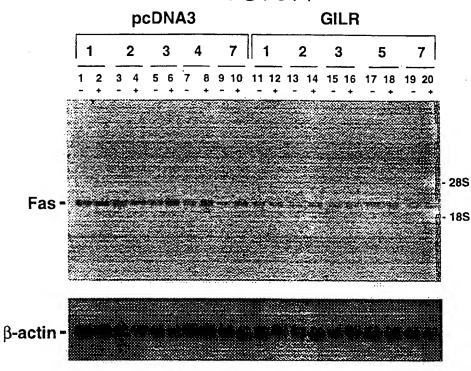
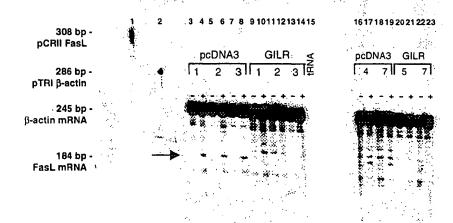


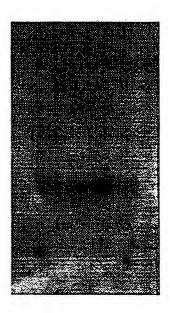
FIG. 9A



F1G.9B



F1G.10A



F1G.10B

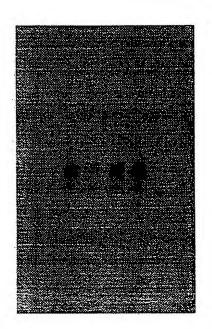
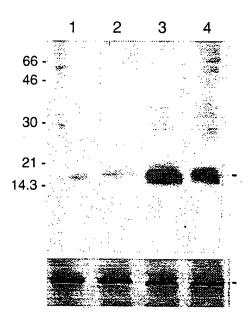
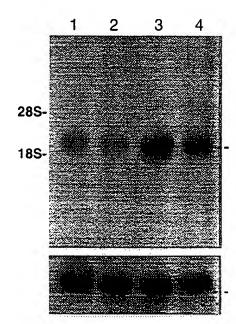
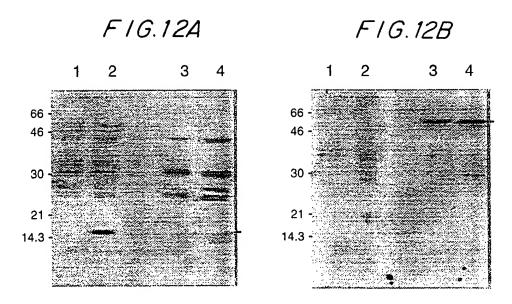


FIG.11A



F/G.11B







F/G.13

- 1 AATTCGGGGGCCGTGGAGTTTGTGACATACGAGGTGACACCCCTCGAGTCACTTCCCTTC
- 61 AACTCCAGCTGGAGCGCCTGCTTGGCTTTGGGTTCGTTCTGCAGCCTTCGCCCCGCTCCT
- 181 AGCCGCCCAGCCCCAGCCCCGCACGAAACCCGGCCAGAGCTTCCTAGCAGCCCGAGCC
- 241 ATGAACACCGAAATGTATCAGACCCCCATGGAGGTGGCGGTCTACCAGCTGCACAATTTC
 MetAsnThrGluMetTyrGlnThrProMetGluValAlaValTyrGlnLeuHisAsnPhe
- 301 TCCATCTCCTTCTCTCTCTCTCTGGAGGGGGATGTGGTTTCCGTTAAGCTGGACAAC SerIleSerPhePheSerSerLeuLeuGlyGlyAspValValSerValLysLeuAspAsn
- 361 AGTGCCTCCGGAGCCAGCGTGGTGGCCATAGACAAGATCGAACAAGGCCATGGATCTG SerAlaSerGlyAlaSerValValAlaIleAspAsnLysIleAspGlnAlaMetAspLeu
- 481 CGAGAGCTGGTGGAGAAGAACTCCCAGCTAGAGCGTGAGAACACCCTGTTGAAGACCCTG
 ArgGluLeuValGluLysAsnSerGlnLeuGluArgGluAsnThrLeuLeuLysThrLeu
- 541 GCAAGCCCAGAGCAGCTGGAGAAGTTCCAGTCCTGTCTGAGCCCTGAAGAGCCAGCTCCC AlaSerProGluGlnLeuGluLysPheGlnSerCysLeuSerProGluGluProAlaPro
- 601 GAATCCCCACAAGTGCCCGAGGCCCCTGGTGGTTCTGCGGTGTAAGTGGCTCTGTCCTCA
 GluSerProGlnValProGluAlaProGlyGlySerAlaVal *
- 721 CAAGCATCATCTCACGAGGAGAACTTTACACCTAGCACAGCTGGTGCCAAGAGATGTCCT
- 781 AAGGACATGGCCACCTGGGTCCACTCCAGCGACAGACCCCTGACAAGAGCAGGTCTCTGG
- 841 AGGCTGAGTTGCATGGGGCCTAGTAACACCAAGCCAGTGAGCCTCTAATGCTACTGCGCC
- 901 CTGGGGGCTCCCAGGGCCTGGGCAACTTAGCTGCCAACTGGCAAAGGAGAAGGGTAGTTTG
- 961 AGGTGTGACACCAGTTTGCTCCAGAAAGTTTAAGGGGTCTGTTTCTCATCTCCATGGACA
- 1021 TCTTCAACAGCTTCACCTGACAACGACTGTTCCTATGAAGAAGCCACTTGTGTTTTAAGC
- 1081 AGAGGCAACCTCTCTCTCTCTCTCTGTTTCGTGAAGGCAGGGGACACAGATGGGAGAGAT
- 1141 TGAGCCAAGTCAGCCTTCTGTTGGTTAATATGGTATAATGCATGGCTTTGTGCACAGCCC
- 1201 AGTGTGGGATTACAGCTTTGGGATGACCGCTTACAAAGTTCTGTTTGGTTAGTATTGGCA
- 1261 TAGTTTTTCTATATAGCCATAAATGCGTATATATACCCATAGGGCTAGATCTGTATCTTA
 1321 GTGTAGCGATGTATACATATACACATCCACCTACATGTTGAAGGGCCTAACCAGCCTTGG
- 1381 GAGTATTGACTGGTCCCTTACCTCTTATGGCTAAGTCTTTGACTGTGTTCATTTACCAAG
- 1441 TTGACCCAGTTTGTCTTTTAGGTTAAGTAAGACTCGAGAGTTAAAGGCAAGGAGGGGGGC
- 1501 CAGCCTCTGAATGCGGCCACGGATGCCTTGCTGCAACCCTTTCCCCAGCTGTCCACCT
- 1561 GAAACGTGAAGTCCTGTTTTGAATGCCAAACCCACCATTCACTGGTGCTGACTACATAGA
- 1621 ATGGGTTGAGAGAAGATCAGTTTGGGCTTCACAGTGTCATTTGAAAAAGCGTTTTTGTTT
- 1681 TGTTTTGAATTATTGTGGAAAACTTTCAAGTGAACAGAAGGATGGTGTCCTACTGTGGAT
- 1741 GAGGGATGAACAAGGGGATGGCTTTGATCCAATGGAGCCTGGGAGGTGTGCCCAGAAAGC
- 1801 TTGTCTGTAGCGGGTTTTGTGAGAGTGAACACTTTCCACTTTTTGACACCTTATCCTGAT
- 1861 GTATGGTTCCAGGATTTGGATTTTCCAAATGTAGCTTGAAATTTCAATAAACTT
- 1921 TGCTCTGTTTTTCTAAAAAATAAAA



F1G.14A

	1CTGGCTGCTGTGGAGTTTGTGACATACTAGGTGACACCCTTGGAGT	C 47
1	[50
48	ACTTCTCTTCAACTCCAGCTTAGAAGTGCCTGCCTGGCTCAGGGTCTGCA	97
51	acttcccttcaactccagctggagcgcctgcttggctttgggttcgtt	98
98	CTGCAGCCTACTCCTTGCTTCAGGGCCTGACTGCAACGCCAAA	140
99	ctgcagccttcgccccgctcctagcctcagggccggactccagcgcagag	148
141		164
149	cccagcccagcctgccagcagccacccagccgcccagccccag	198
165	GCAGCCACTCAAACCAGCCACAGCTCCCCGGCA.ACCGAACCATGAACAC	213
199	$\verb ccccgcacgaaacccggccagagcttcctagcagcccgagccatgaacac $	248
214	CGAAATGTATCAGACCCCCATGGAGGTGGCGGTCTATCAGCTGCACAATT	263
249		298
264	TCTCCACCTCCTTCTTTCTCTCTCTGGAGGGGATGTGGTTTCCGTT	313
299		348
314	AAACTGGATAACAGTGCCTCCGGAGCCAGTGTGGTGGCCCTAGACAACAA	363
349	aagctggacaacagtgcctccggagccagcgtggtggccatagacaacaa	398
364	GATTGAGCAGGCCATGGACCTCGTGAAGAACCACCTGATGTACGCTGTGA	413
399		448
414	GAGAGGAGGTGGAGGTCCTAAAGGAGCAGATTCGTGAGCTGCTTGAGAAG	463
449		498
464	AACTCCCAGCTGGAGCGCGAGAACACCCTCCTGAAGACGCTGGCAAGCCC	513
499		548
514	CGAGCAACTGGAAAAGTTCCAGTCCCGGCTGAGCCCTGAAGAGCCAGCAC	563
549	agagcagctggagaagttccagtcctgtctgagccctgaagagccagctc	598
564	CTGAAGCCCCAGAAACCCCGGAAGCCCCTGGTGGTTCTGCG	613
599		639

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3,				*/
13	70 .	n.E	11,	

F	IG.	14B
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014		661
640	gtgtaagtggctctgtcctcagggtgggcagagccactaaacttgttta	689
662	CCTAGTTCTTTCCAGTTTGTTTTTTGGCTCCCCAAGGGTCATCTCATGTGG	711
690		739
712	AGAACTTTACACCTAACATAGCTGGTGCCAAGAGATGTCCCAAGGACATG	761
740	agaactttacacctagcacagctggtgccaagagatgtcctaaggacatg	789
762	CCCATCTGGGTCCACTCCAGTGACAGACCCCTGACAAAGAGCAGGTCTCT	811
790	gccacctgggtccactccagcgacagacccctgac.aagagcaggtctct	838
812	GGAGACTAAGTTGCATGGGGCCTAGTAACACCAAGCCAGTGAGCCTGTCG	861
839		888
862	TGTCACCGGGCCCTGGGGGCTCCCAGGG.CTGGGCAACTTAGTTACAGCT	910
889	tgctactgcgccctgggggctcccagggcctgggcaacttagctgcaact	938
911	GACCAAGGAGAAAGTAGTTTTGAGATGTGATGCCAGTGTGCTCCAGAAAG	960
939		988
961	TGTAAGGGGTCTGTTTTCCATTGACATCTTCCACAGCTTCACCT	1010
989	tttaaggggtctgtttctcatctccatggacatcttcaacagcttcacct	1038
1011	GACAATGACTGTTCCTATGAAGAAGCCACTTGTGTTCTAAGCAGAAGCAA	1060
	gacaacgactgttcctatgaagaagccacttgtgttttaagcagaggcaa	1088
	CCTCTCTCTTCTCTCTCTTTTCCAGGCAGGGG.CAGAGATGGGAGA	1109
	cctctcttc.tcctctgtttcgtgaaggcaggggacacagatgggaga	1137
	GATTGAGCCAAATGAGCCTTCTGTTGGTTAATACTGTATAATGCATGGCT	1159
1138	<pre>gattgagccaagtcagccttctgttggttaatatggtataatgcatggct</pre>	1187
1160	TTGTGCACAGCCCAGTGTGGGGTTACAGCTTTTGGGATGACTGCTTATAAA	1209
1188	ttgtgcacagccagtgtgggattacagctttgggatgaccgcttacaaa	1237
1210	GTTCTGTTTGGTTAGTATTGGCATCGTTTTTCTATATAGCCAT.AATGCG	1258
1238		1287
1259	TATATATACCCATAGGGCTAGATCTATATCTTAGGGTAGTGATGTATACA	1308
1288	tatatatacccatagggctagatctgtatcttagtgtagcgatgtataca	1337



F1G.14C

1309	TATACACATACACCTACATGTTGAAGGGCCTAACCAGCTTTGGGAGTACT	1358
1338	tatacacatccacctacatgttgaagggcctaaccagccttgggagtatt	1387
1359	GACTGGTCTCTTATCTCTTAAAGCTAAGTTTTTGACTGTGCTAATTTACC	1408
1388	gactggtcccttacctcttatggctaagtctttgactgtgttcatttacc	1437
1409	AAATTGATCCAGTTTGTCCTTTAGATTAAATAAG.ACTCGATATGAGGGA	1457
1438	aagttgacccagtttgtcttttaggttaagtaagaactcgagagtaaagg	1487
1458	GGGAGGGGAAGACCAGCCTCACAATGCGGCCACAGATGCCTTGCTGCTGC	1507
1488	caaggagggggccagcctctgaatgcggccacggatgccttgctgc	1537
1508	AGTCC.TCCTGATCTGTCCACTGAAGACATGAAGTCCTCTTTTGAATGC	1556
1538	aaccetttcccagetgtccactgaa.acgtgaagtcctgttttgaatgc	1586
1557	CAAACCCACCATTCATTGGTGCTGACTACATAGAATGGGGTTGAGAGAG	1606
1587	caaacccaccattcactggtgctgactacatagaat.gggttgagagaag	1635
	ATCAGTTTGGACTTCACATTTTTGTTTTAAGTTTTAGGTTGTTTTTTTT	1656
1636		1680
1657	GGTTTTGTTTGTTTGTTTGTTTTTTTTTTTTTTTTTTTT	1706
1681	tgttttgaattattgt	1696
1707	TTAAGTTCTTGTGGGGAAACTTTGGGGTTAATCAAAGGATGTAGTCCTGT	1756
1697		1733
1757	GGTAGACCAGAGGAGTAACTAGTTTTGATCCTTTGGGGTGTGGA	1800
1734		1783
1801	AAATGTACCCAGGAAGCTTGTGT.AAGGAGGTTCTGTGACAGTGAACACT	1849
1784		1833
1850		1899
1834		1883
1900	GGATTTTTCAAATGTAGCTTGAAATTTCAATAAACTTTGCTCCTTTTTCT	1949
1884		1933
1950	ААААТААААААААААААА	
1934		



F1G.15

mG	1	MNTEMYQTPMEVAVYQLHNFSTSFFSSLLGGDVVSVKLDNSASGASVVAL	50
hG	1	MNTEMYQTPMEVAVYQLHNFSISFFSSLLGGDVVSVKLDNSASGASVVAI	50
hT	2	KSQWCRPVAMDLGVYQLRHFSISFLSSLLGTENASVRLDNSSSGASVVAI	51
mG	51	DNKIEQAMDLVKNHLMYAVREEVEVLKEQIRELLEKNSQLERENTLLKTL	100
hG	51	DNKIEQAMDLVKNHLMYAVREEVEILKEQIRELVEKNSQLERENTLLKTL	100
hΤ	52	DNKIEQAMDLVKSHLMYAVREEVEVLKEQIKELIEKNSQLEQENNLLKTL	101
hD	1	MDLVKNHLMYAVREEVEILKEQIRELVEKNSQLERENTLLKTL	43
mG	101	ASPEQLEKFQSRLSPEEPAPEAPETPETPEAPGGSAV*	137
hG	101	ASPEQLEKFQSCLSPEEPAPESPQVPEAPGGSAV*	134
hΤ	102	ASPEQLAQFQAQLQTGSPPATTQPQGTTQPPAQPASQGSGPTA*	144
hD	44	ASPEQLEKFQSCLSPEEPAPESPQVPEAPGGSAV*	77

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